

## SEQUENCE LISTING

<110> National Research Council of Canada

<120> FATTY ACID ELONGASE (FAE) GENES AND THEIR UTILITY IN INCREASING ERUCIC ACID AND OTHER VERY LONG-CHAIN FATTY ACID PROPORTIONS IN SEED OIL

<130> PAT 989W-90

<140> Unknown

<141> 2004-11-24

<150> US 60/524,645

<151> 2003-11-25

<160> 27

<170> PatentIn version 3.2

<210> 1

<211> 18

<212> DNA

<213> Artificial

<220>

<223> F1 Forward Primer

<400> 1

tctwggwggm atggggttg

18

<210> 2

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Coded by F1 Forward Primer

<400> 2

Leu Gly Gly Met Gly Cys

1

5

<210> 3

<211> 18

<212> DNA

<213> Artificial

<220>

<223> R1 Reverse Primer

<400> 3

trtaygcyar ctcttacc

18

<210> 4  
<211> 6  
<212> PRT  
<213> Artificial

<220>  
<223> Coded by R1 Reverse Primer

<400> 4

Trp Tyr Glu Leu Ala Tyr  
1 5

<210> 5  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> P Forward Primer

<400> 5

accatgtcag gaacaaaagc 20

<210> 6  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> PR Reverse Primer

<400> 6

ttaatttaat ggaacctcaa ccg 23

<210> 7  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> F2 Forward Primer

<400> 7

tcgaggatgt cgcttcaccg atttggaac ac 32

<210> 8  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> R2 Reverse Primer

<400> 8

gtttccaaat cggatgaagcg acatcctcga tgg 33

<210> 9

<211> 25

<212> DNA

<213> Artificial

<220>

<223> F3 Forward Primer

<400> 9

taggatccat gtcaggaaca aaagc 25

<210> 10

<211> 30

<212> DNA

<213> Artificial

<220>

<223> R3 Reverse Primer

<400> 10

tagagctctt aatttaatgg aacctcaacc 30

<210> 11

<211> 30

<212> DNA

<213> Artificial

<220>

<223> R4 Reverse Primer

<400> 11

taggatcctt aatttaatgg aacctcaacc 30

<210> 12

<211> 17

<212> DNA

<213> Artificial

<220>

<223> F4 Forward Primer

<400> 12

atgtcaggaa caaaagc 17

<210> 13

<211> 22

<212> DNA  
<213> Artificial

<220>  
<223> R5 Reverse Primer

<400> 13

taattttaatg gaacctcaac cg 22

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> F5 Forward Primer

<400> 14

gcaatgacgt ccattaacgt aaag 24

<210> 15  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> R6 Reverse Primer

<400> 15

ttaggaccga ccgttttggg c 21

<210> 16  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<223> F6 Forward Primer

<400> 16

tatctagaat gacgtccatt aacgtaaag 29

<210> 17  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> R7 Reverse Primer

<400> 17

atggtacctt aggaccgacc gtttttg 27

<210> 18  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> NN-3 Primer

<400> 18

tttcttcgcc acttgtcact cc 22

<210> 19  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> NN-4 Primer

<400> 19

cgcgctatat tttgttttct a 21

<210> 20  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> OM087 Primer

<400> 20

agagagaggg atccatgagt gtgataggta gg 32

<210> 21  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> OM088 Primer

<400> 21

gaggaagaag gatccgggtc tatatactac tct 33

<210> 22  
<211> 503  
<212> PRT  
<213> Tropaeolum majus

&lt;400&gt; 22

Met Ser Gly Thr Lys Ala Thr Ser Val Ser Val Pro Leu Pro Asp Phe  
 1 5 10 15  
 Lys Gln Ser Val Asn Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Ser  
 20 25 30  
 Ile Thr His Ala Met Tyr Leu Phe Leu Thr Pro Leu Leu Ile Met  
 35 40 45  
 Ser Ala Gln Ile Ser Thr Phe Ser Ile Gln Asp Phe His His Leu Tyr  
 50 55 60  
 Asn His Leu Ile Leu His Asn Leu Ser Ser Leu Ile Leu Cys Ile Ala  
 65 70 75 80  
 Leu Leu Leu Phe Val Leu Thr Leu Tyr Phe Leu Thr Arg Pro Thr Pro  
 85 90 95  
 Val Tyr Leu Leu Asn Phe Ser Cys Tyr Lys Pro Asp Ala Ile His Lys  
 100 105 110  
 Cys Asp Arg Arg Arg Phe Met Asp Thr Ile Arg Gly Met Gly Thr Tyr  
 115 120 125  
 Thr Glu Glu Asn Ile Glu Phe Gln Arg Lys Val Leu Glu Arg Ser Gly  
 130 135 140  
 Ile Gly Glu Ser Ser Tyr Leu Pro Pro Thr Val Phe Lys Ile Pro Pro  
 145 150 155 160  
 Arg Val Tyr Asp Ala Glu Glu Arg Ala Glu Ala Glu Met Leu Met Phe  
 165 170 175  
 Gly Ala Val Asp Gly Leu Phe Glu Lys Ile Ser Val Lys Pro Asn Gln  
 180 185 190  
 Ile Gly Val Leu Val Val Asn Cys Gly Leu Phe Asn Pro Ile Pro Ser  
 195 200 205  
 Leu Ser Ser Met Ile Val Asn Arg Tyr Lys Met Arg Gly Asn Val Phe  
 210 215 220  
 Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ser Ile  
 225 230 235 240  
 Asp Leu Ala Lys Asp Leu Leu Gln Val Arg Pro Asn Ser Tyr Ala Leu  
 245 250 255  
 Val Val Ser Leu Glu Cys Ile Ser Lys Asn Leu Tyr Leu Gly Glu Gln  
 260 265 270  
 Arg Ser Met Leu Val Ser Asn Cys Leu Phe Arg Met Gly Gly Ala Ala  
 275 280 285  
 Ile Leu Leu Ser Asn Lys Met Ser Asp Arg Trp Arg Ser Lys Tyr Arg  
 290 295 300

Leu Val His Thr Val Arg Thr His Lys Gly Thr Glu Asp Asn Cys Phe  
 305 310 315 320  
 Ser Cys Val Thr Arg Lys Glu Asp Ser Asp Gly Lys Ile Gly Ile Ser  
 325 330 335  
 Leu Ser Lys Asn Leu Met Ala Val Ala Gly Asp Ala Leu Lys Thr Asn  
 340 345 350  
 Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu  
 355 360 365  
 Phe Phe Ala Thr Leu Val Gly Lys Lys Val Phe Lys Met Lys Leu Gln  
 370 375 380  
 Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys Ile His  
 385 390 395 400  
 Ala Gly Gly Arg Ala Val Leu Asp Glu Leu Glu Lys Asn Leu Lys Leu  
 405 410 415  
 Ser Ser Trp His Met Glu Pro Ser Arg Met Ser Leu Tyr Arg Phe Gly  
 420 425 430  
 Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ser Glu Ala  
 435 440 445  
 Lys Gly Arg Ile Lys Lys Gly Asp Arg Val Trp Gln Ile Ala Phe Gly  
 450 455 460  
 Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg Asn Val  
 465 470 475 480  
 Asn Pro Ala Glu Glu Lys Asn Pro Trp Met Asp Glu Ile His Leu Phe  
 485 490 495  
 Pro Val Glu Val Pro Leu Asn  
 500

<210> 23  
 <211> 1765  
 <212> DNA  
 <213> Tropaeolum majus

<400> 23

agtttttttt gttgagaata accatgtcag gaacaaaagc aacatcagtt tctgttccac 60  
 tgcttgattt caagcaatca gttaatctaa aatatgttaa acttggttat cattactcga 120  
 tcactcatgc aatgtatctt tttctaacc cttctcttct cataatgtct gctcaaactct 180  
 caactttctc tattcaagat tttcaccatc tttataacca tcttatactc cacaatctct 240  
 catcccttat cctatgcac gctctctctc tcttcgtctt aaccctctat ttccttactc 300  
 gtcccacgcc tgtttattta ctcaacttct cttgttataa accggatgct attcacaaat 360  
 gcgaccgccg tcgtttcatg gacaccattc gtggaatggg tacttatacg gaagagaaca 420

```

tcgagtttca aaggaaagtt ctagaaaggt ccggaatagg ggaatcgtct tatcttcctc 480
cgactgtggt taaaattcct cctagggttt acgatgcgga ggaacgcgcg gaggctgaga 540
tgctgatggt cgggtgcggt gatgggcttt tcgagaaaat atctgttaaa ccgaatcaaa 600
tcgggggttt ggttggtgaat tgtgggttgt ttaatccgat accgtcttta tcttccatga 660
ttgtgaatcg ctacaagatg agagggaatg tttttagtta taatttgggt ggaatggggt 720
gtagtgcggg tgtgatttcg attgatcttg ctaaagatct tcttcagggt cgtcccaact 780
catatgcttt ggtgggttagt ttggaatgta tctcgaagaa cttgtatctc ggtgaacaaa 840
gatcgatgct tgtttccaac tgtttgtttc gaatgggtgg ggcggcgatt ttgctttcga 900
ataaaatgtc ggatcgatgg agatcaaagt atagattggt tcatacgggt cgaaccacaca 960
aggggtaccga ggataactgc ttttcttgcg taactagaaa ggaagactcg gacgggaaga 1020
tcgggtatttc tttatcgaag aacctaatgg ctgttgccgg agacgcattg aagactaata 1080
tcacaaccct cggaccactt gttctacca tgtcggaaca attactcttc ttcgctactt 1140
tggtcggaaa aaagggttttc aagatgaagc tacagccgta tataccggat ttcaagttgg 1200
ctttcgagca tttctgtatt catgcagggt gaagagctgt tctggatgaa ttggagaaga 1260
acttgaagct ttcgagttgg catatggaac catcgaggat gtcgctttac cgatttggaa 1320
acacgtcgag tagttcgctt tggtagcagt tggcttattc ggaggcgaaa gggagaataa 1380
agaagggaga tcgagtatgg caaatcgcgt ttgggtcggg atttaagtgt aacagtgcgg 1440
tgtggaaggc tctaaggaat gttaatccgg cggaagagaa aaatccttgg atggatgaga 1500
ttcacctatt tccggttgag gttccattaa attaaaacct atcttcaagt tacaagttgt 1560
tgttgttggt tcattaggtt taataataag ctaatatgga aagcctttct actctctttt 1620
ttttccactt ttttttttca atttcagagt tgggtcttag ttgtatcatc tacatgagtg 1680
tattcgctat gcgctattcg ctattcgcta ttcactagtt aataaaatca aacgtccaaa 1740
aaaaaaaaa aaaaaaaaaa aaaaa 1765

```

```

<210> 24
<211> 506
<212> PRT
<213> Crambe abyssinica

```

```

<400> 24

```

```

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
1           5           10           15

```

```

Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
          20           25           30

```



Ala Ser Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr  
                   35                  40                  45  
 Leu Gln His Asn Val Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val  
           50                  55                  60  
 Phe Gly Ser Ile Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu  
   65                  70                  75                  80  
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr Gln Cys Arg Ser Ser Ile  
                   85                  90                  95  
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Phe  
                  100                 105                 110  
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys  
          115                 120                 125  
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly  
          130                 135                 140  
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu  
  145                 150                 155                 160  
 Thr Glu Gln Val Ile Val Gly Ala Leu Lys Asn Leu Phe Glu Asn Thr  
                  165                 170                 175  
 Lys Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met  
                  180                 185                 190  
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
          195                 200                 205  
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser  
  210                 215                 220  
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
  225                 230                 235                 240  
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn  
                  245                 250                 255  
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe  
                  260                 265                 270  
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg  
          275                 280                 285  
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly  
  290                 295                 300  
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn  
  305                 310                 315                 320  
 Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Glu Val Ala Gly  
                  325                 330                 335  
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
                  340                 345                 350

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Ala Lys Lys Leu  
 355 360 365  
 Phe Lys Asp Lys Val Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
 370 375 380  
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val  
 385 390 395 400  
 Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala Ser Arg  
 405 410 415  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
 420 425 430  
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys  
 435 440 445  
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val  
 450 455 460  
 Trp Val Ala Leu Ser Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu  
 465 470 475 480  
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Ala Lys  
 485 490 495  
 Ser Glu Thr Arg Ala Gln Asn Gly Arg Ser  
 500 505

<210> 25  
 <211> 1521  
 <212> DNA  
 <213> *Crambe abyssinica*

<400> 25

atgacgtcca ttaacgtaaa gctcctttac cattacgtca taaccaacct tttaacctc 60  
 tgtttctttc cgtaacggc gatcgctgcc gggaaagcct ctcggttac catagacgat 120  
 cttcaccact tatattattc ctatctccaa cacaacgtca taaccatagc tccactcttt 180  
 gcctttaccg ttttcggttc gattctctac atcgtgacct ggcccaaacc ggtttacctc 240  
 gttgagtact catgctacct tccaccaacg cagtgtagat caagtatctc caaggctcatg 300  
 gatataatatt atcaagtaag aaaagctgat ctttttcgta acgggacatg cgatgactcg 360  
 tcctggcttg acttcttgag gaagattcaa gaacgttcag gtctaggcga cgaaactcac 420  
 ggccccgagg gactgcttca ggtccctccc cggaagactt ttgcggcggc gcgtgaagag 480  
 acggagcaag taatcgctcg tgcgctgaaa aatctattcg agaacaccaa agttaaccct 540  
 aaagatatag gtatacttgt ggtgaactca agcatgttta atccaactcc ttcactctca 600  
 gcgatggctc ttaatacttt caagctccga agtaacgtaa gaagctttaa ccttggtggc 660

```

atggggttgta gtgctggcgt tatagccatt gatctggcta aggacttggt gcatgtccat    720
aaaaacacgt atgctcttgt ggtgagcaca gagaacatca cttataacat ttacgctggc    780
gataatagat ccatgatggg ttcaaactgc ttgttccgtg ttggcggggc cgctattttg    840
ctctccaaca agcctagaga tcgaagacgg tccaaatacg agctagttca cacggtccga    900
acacataccg gagctgatga caagtctttc cgatgcgtcc aacaaggaga cgatgagaac    960
ggcaaaaccg gagtgagttt gtccaaggac ataaccgagg ttgctggtcg aacggttaag   1020
aaaaacatag caacattggg tcctttgatt cttcctttta gcgagaaact tctttttttc   1080
gttaccttca tggccaagaa acttttcaaa gataaagtta agcattacta tgtcccggac   1140
ttcaagcttg ctattgacca tttttgtata catgcgggag gcagagccgt gatcgatgtg   1200
ctagagaaga atttaggcct agcaccgatc gatgtagagg catcaagatc aacgttacat   1260
agatttggtg acacatcatc tagctcaata tggtatgagt tggcatacat agaggcaaaa   1320
ggaaggatga agaaaggtaa taaagtttg cagattgctt tagggtcagg ctttaagtgt   1380
aacagtgcgg tttgggtagc tttaagcaat gtcaaggctt cgacaaatag tccttgggaa   1440
cattgcatcg atagataccc ggttaaaatt gattctgatt cagctaagtc agagactcgt   1500
gcccaaaacg gtcggtccta a                                     1521

```

<210> 26  
 <211> 506  
 <212> PRT  
 <213> Arabidopsis sp.

<400> 26

```

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1          5          10          15

Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20          25          30

Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35          40          45

Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50          55          60

Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65          70          75          80

Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
85          90          95

Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100         105         110

```

Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys  
 115 120 125  
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly  
 130 135 140  
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu  
 145 150 155 160  
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr  
 165 170 175  
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met  
 180 185 190  
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys  
 195 200 205  
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser  
 210 215 220  
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His  
 225 230 235 240  
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly  
 245 250 255  
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe  
 260 265 270  
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg  
 275 280 285  
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly  
 290 295 300  
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser  
 305 310 315 320  
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly  
 325 330 335  
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro  
 340 345 350  
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu  
 355 360 365  
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala  
 370 375 380  
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu  
 385 390 395 400  
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg  
 405 410 415  
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr  
 420 425 430



ttcaagcttg	ctgttgacca	tttctgtatt	catgccggag	gcagagccgt	gatcgatgag	1200
ctagagaaga	acttaggact	atcgccgata	gatgtggagg	catctagata	aacggtacat	1260
agatttggga	atacttcata	tagctcaatt	tggtatgaat	tagcatacat	agaggcaaag	1320
ggaagaatga	agaaagggaa	taaagcttgg	cagattgctt	taggatacag	gtttaagtgt	1380
aatagtgcgg	tttgggtggc	tctacgcaat	gtcaaggcat	cggcaaatag	tccttggcaa	1440
cattgcatcg	atagatatcc	ggttaaaatt	gattctgatt	tgtcaaagtc	aaagactcat	1500
gtccaaaacg	gtcggtccta	a				1521